



#6

-1-

SEQUENCE LISTING

A2

<110> Hanke, Paul D.

<120> Feedback-Resistant Pyruvate Carboxylase Gene from *Corynebacterium*

<130> 1533.1230001/MAC/RGM

<140> US 09/974,973

<141> 2001-10-12

<150> US 60/239,913

<151> 2000-10-13

Sub B15

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<170> PatentIn version 3.0

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<212> DNA

<213> *Corynebacterium glutamicum*

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Tyr Val Glu Arg Ala Val 225	Ile 230	Asn Pro Gln His 235	Ile Glu Val Gln Ile 240	
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His Leu Asp Pro Glu Leu Arg 275	Asp 280	Arg Ile Cys Ala Asp 285	Ala Val Lys	
Phe Cys Arg Ser Ile Gly Tyr 290	Gln Gly Ala Gly 300	Thr Val Glu Phe Leu		

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740 745 750

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Gly Ser Phe His Arg Ser Phe Ala Ser Glu Ala Val Arg Ile Gly Thr
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Glu Gly Ser Pro Val Lys Ala Tyr Leu Asp Ile Asp Glu Ile Ile Gly
85 90 95
Ala Ala Lys Lys Val Lys Ala Asp Ala Ile Tyr Pro Gly Tyr Gly Phe

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Ala	Thr	Tyr	Phe	Ala	Ala	Ala	Gln	Ala	Gly	Ala	Asp	Ala	Val	Asp	Gly	770	775	780
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Ser Phe His Arg Ser Phe Ala Ser Glu Ala Val Arg Ile Gly Thr Glu
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Gly Ser Pro Val Lys Ala Tyr Leu Asp Ile Asp Glu Ile Ile Gly Ala
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Ala Lys Lys Val Lys Ala Asp Ala Ile Tyr Pro Gly Tyr Gly Phe Leu
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Ser Glu Asn Ala Gln Leu Ala Arg Glu Cys Ala Glu Asn Gly Ile Thr
100 105 110

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Glu	Val	Ala	Met	Ala	Tyr	Ser	Gly	Asp	Leu	Ser	Asp	Pro	Asn	Glu	Lys
		675					680					685			
Leu	Tyr	Thr	Leu	Asp	Tyr	Tyr	Leu	Lys	Met	Ala	Glu	Glu	Ile	Val	Lys
	690					695					700				
Ser	Gly	Ala	His	Ile	Leu	Ala	Ile	Lys	Asp	Met	Ala	Gly	Leu	Leu	Arg
705					710					715					720
Pro	Ala	Ala	Val	Thr	Lys	Leu	Val	Thr	Ala	Leu	Arg	Arg	Glu	Phe	Asp
				725					730					735	
Leu	Pro	Val	His	Val	His	Thr	His	Asp	Thr	Ala	Gly	Gly	Gln	Leu	Ala
			740					745					750		
Thr	Tyr	Phe	Ala	Ala	Ala	Gln	Ala	Gly	Ala	Asp	Ala	Val	Asp	Gly	Ala
		755					760					765			
Ser	Ala	Pro	Leu	Ser	Gly	Thr	Thr	Ser	Gln	Pro	Ser	Leu	Ser	Ala	Ile
	770					775					780				

Val	Ala	Ala	Phe	Ala	His	Thr	Arg	Arg	Asp	Thr	Gly	Leu	Ser	Leu	Glu	785	790	795	800
Ala	Val	Ser	Asp	Leu	Glu	Pro	Tyr	Trp	Glu	Ala	Val	Arg	Gly	Leu	Tyr	805	810	815	
Leu	Pro	Phe	Glu	Ser	Gly	Thr	Pro	Gly	Pro	Thr	Gly	Arg	Val	Tyr	Arg	820	825	830	
His	Glu	Ile	Pro	Gly	Gly	Gln	Leu	Ser	Asn	Leu	Arg	Ala	Gln	Ala	Thr	835	840	845	
Ala	Leu	Gly	Leu	Ala	Asp	Arg	Phe	Glu	Leu	Ile	Glu	Asp	Asn	Tyr	Ala	850	855	860	
Ala	Val	Asn	Glu	Met	Leu	Gly	Arg	Pro	Thr	Lys	Val	Thr	Pro	Ser	Ser	865	870	875	880
Lys	Val	Val	Gly	Asp	Leu	Ala	Leu	His	Leu	Val	Gly	Ala	Gly	Val	Asp	885	890	895	
Pro	Ala	Asp	Phe	Ala	Ala	Asp	Pro	Gln	Lys	Tyr	Asp	Ile	Pro	Asp	Ser	900	905	910	
Val	Ile	Ala	Phe	Leu	Arg	Gly	Glu	Leu	Gly	Asn	Pro	Pro	Gly	Gly	Trp	915	920	925	
Pro	Glu	Pro	Leu	Arg	Thr	Arg	Ala	Leu	Glu	Gly	Arg	Ser	Glu	Gly	Lys	930	935	940	
Ala	Pro	Leu	Thr	Glu	Val	Pro	Glu	Glu	Glu	Gln	Ala	His	Leu	Asp	Ala	945	950	955	960
Asp	Asp	Ser	Lys	Glu	Arg	Arg	Asn	Ser	Leu	Asn	Arg	Leu	Leu	Phe	Pro	965	970	975	
Lys	Pro	Thr	Glu	Glu	Phe	Leu	Glu	His	Arg	Arg	Arg	Phe	Gly	Asn	Thr	980	985	990	
Ser	Ala	Leu	Asp	Asp	Arg	Glu	Phe	Phe	Tyr	Gly	Leu	Val	Glu	Gly	Arg	995	1000	1005	
Glu	Thr	Leu	Ile	Arg	Leu	Pro	Asp	Val	Arg	Thr	Pro	Leu	Leu	Val		1010	1015	1020	
Arg	Leu	Asp	Ala	Ile	Ser	Glu	Pro	Asp	Asp	Lys	Gly	Met	Arg	Asn		1025	1030	1035	
Val	Val	Ala	Asn	Val	Asn	Gly	Gln	Ile	Arg	Pro	Met	Arg	Val	Arg		1040	1045	1050	
Asp	Arg	Ser	Val	Glu	Ser	Val	Thr	Ala	Thr	Ala	Glu	Lys	Ala	Asp		1055	1060	1065	
Ser	Ser	Asn	Lys	Gly	His	Val	Ala	Ala	Pro	Phe	Ala	Gly	Val	Val		1070	1075	1080	
Thr	Val	Thr	Val	Ala	Glu	Gly	Asp	Glu	Val	Lys	Ala	Gly	Asp	Ala		1085	1090	1095	
Val	Ala	Ile	Ile	Glu	Ala	Met	Lys	Met	Glu	Ala	Thr	Ile	Thr	Ala		1100	1105	1110	

A2
cont.

Ser	Val	Asp	Gly	Lys	Ile	Asp	Arg	Val	Val	Val	Pro	Ala	Ala	Thr
1115						1120					1125			
Lys	Val	Glu	Gly	Gly	Asp	Leu	Ile	Val	Val	Val	Ser			
1130						1135					1140			
